

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Selifonov et al.

Attorney Docket No.:
MXGNP002X1/0159.210

Application No.: 09/495,668

Examiner: Kim J. Young

Filed: February 1, 2000

Group: 1631

Title: METHODS OF POPULATING DATA
STRUCTURES FOR USE IN
EVOLUTIONARY SIMULATIONS

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the U.S. Postal Service with sufficient postage as priority mail on January 9, 2004 in an envelope addressed to the Commissioner for Patents, P.O. Box 1450 Alexandria, VA 22313-1450.

Signed: _____

Leslie Russell

**INFORMATION DISCLOSURE STATEMENT
37 CFR §§1.56 AND 1.97(b)**

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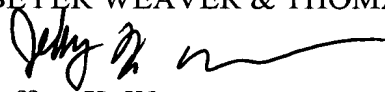
Dear Sir:

The references listed in the attached PTO Form 1449, copies of which are attached, may be material to examination of the above-identified patent application. Applicants submit these references in compliance with their duty of disclosure pursuant to 37 CFR §§1.56 and 1.97. The Examiner is requested to make these references of official record in this application.

This Information Disclosure Statement is not to be construed as a representation that a search has been made, that additional information material to the examination of this application does not exist, or that these references indeed constitute prior art.

This Information Disclosure Statement is: (i) filed within three (3) months of the filing date of the above-referenced application, (ii) believed to be filed before the mailing date of a first Office Action on the merits, or (iii) believed to be filed before the mailing of a first Office Action after the filing of a Request for Continued Examination under §1.114. Accordingly, it is believed that no fees are due in connection with the filing of this Information Disclosure Statement. However, if it is determined that any fees are due, the Commissioner is hereby authorized to charge such fees to Deposit Account 500388 (Order No. MXGNP002X1).

Respectfully submitted,
BEYER WEAVER & THOMAS, LLP



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Form 1449 (Modified)

Information Disclosure Statement By Applicant

(Use Several Sheets if Necessary)

Atty Docket No. MXGNP002X1/0159.210US

Applicant: Selifonov et al.

Filing Date February 1, 2000

Application No.: 09/495,668

Group 1637

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Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Aita et al., "Analysis of Local Fitness Landscape with a Model of the Rough Mt. Fuji-Type Landscape: Application to Prolyl Endopeptidase and Thermolysin," Biopolymers. Vol. 54, pp. 64-79, Accepted January 14, 2000
	C2	Hellberg et al., "The Prediction of Bradykinin Potentiating Potency of Pentapeptides. An Example of a Peptide Quantitative Structure-Activity Relationship," Acta Chemica Scandinavica B 40, pp. 135-140, 1988
	C3	Bucht et al., "Optimising the Signal Peptide for Glycosyl Phosphatidylinositol Modification of Human Acetylcholinesterase Using Mutational Analysis and Peptide-Quantitative Structure-Activity Relationships," Biochimica et Biophysica Acta 1431, pp. 471-482, 1999
	C4	Sandberg et al., "Engineering Multiple Properties of a Protein by Combinatorial Mutagenesis," Proc. Natl. Acad. Sci. USA, Vol. 90, pp. 8367-8371, September 1993
	C5	Wrede et al., "Peptide Design Aided by Neural Networks: Biological Activity of Artificial Signal Peptidase I Cleavage Sites," Biochemistry, 37, pp. 3588-3593, 1998
	C6	Jill Damborsky, "Quantitative Structure-Function and Structure-Stability Relationships of Purposely Modified Proteins," Protein Engineering, Vol. 11, no. 1, pp. 21-30, 1998
	C7	Hellberg, et al., "Peptide Quantitative Structure-Activity Relationships, a Multivariate Approach," J. Med Chem, 30: pp 1126-1195, 1987
	C8	Sandberg et al., "New Chemical Descriptors Relevant for the Design of Biologically Active Peptides. A Multivariate Characterization of 87 Amino Acids," J. Med Chem., 41, pp. 2481-2491, 1998
	C9	Casari et al., "A Method to Predict Functional Residues in Proteins," Nat. Struct Biol., 2, pp. 171-178, 1995
	C10	Gogos et al., "Assignment of Enzyme Substrate Specificity by Principal Component Analysis of Aligned Protein Sequences: An Experimental Test Using DNA Glycosylase Homologs," Proteins: Structure, Function, and Genetics, 40, pp. 98-105, 2000
	C11	Suzuki et al., "A Method for Detecting Positive Selection at Single Amino Acid Sites," Mol. Biol. Evol. 16 (10): pp. 1315-1328, 1999
	C12	Benner et al., "Amino Acid Substitution During Functionally Constrained Divergent Evolution of Protein Sequences," Protein Engineering, Vol. 7, No. 11, pp. 1323-1332, 1994

Form 1449 (Modified) Information Disclosure Statement By Applicant (Use Several Sheets if Necessary)	Atty Docket No.	Application No.:
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	Applicant:	
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	C13	Wu et al., "Discovering Empirically Conserved Amino Acid Substitution Groups in Databases of Protein Families," Proc. Int. Conf. Intell. Syst. Mol. Biol., 4, pp. 230-240, 1996
	C14	Adenot et al., "Peptides Quantitative Structure-Function Relationships: An Automated Mutation Strategy to Design Peptides and Pseudopeptides from Substitution Matrices," Journal of Molecular Graphics and Modelling, 17, pp. 292-309, 1999
	C15	Norinder et al., "A Quantitative Structure-Activity Relationship Study of Some Substance P-Related Peptides," J. Peptide Res., 49, pp. 155-162, 1997
	C16	Sandberg, "Deciphering Sequence Data a Multivariate Approach," Ph.D Thesis, Umea: Umea University, 78 pages, 1997
	C17	Eriksson et al., "Peptide QSAR on Substance P Analogues, Enkephalins and Bradykinins Containing L-and D-Amino Acids," Acta Chemica Scandinavica, 44, pp. 50-56, 1990
	C18	Ufkes et al., "Further Studies on the Structure-Activity Relationships of Bradykinin-Potentiating Peptides," European Journal of Pharmacology, 79, pp. 155-158, 1982
	C19	Dobrynin et al., "Synthesis of Model Promoter for Gene Expression in Escherichia Coli," Symposium Series No. 7, pp. 365-376, 1980
	C20	Skinner et al., "Potential Use of Additivity of Mutational Effects in Simplifying Protein Engineering," Proc. Natl. Acad. Sci., Vol. 93, pp. 10753-10757, 1996
	C21	Aita et al., "Theory of Evolutionary Molecular Engineering Through Simultaneous Accumulation of Advantageous Mutations," J. Theor. Biol., 207, pp/ 543-556, 2000
	C22	Lathrop et al., "Global Optimum Protein Threading with Gapped Alignment and Empirical Pair Score Functions," J. Mol. Biol., 255, pp. 641-665, 1996
	C23	Hellberg et al., "A Multivariate Approach to QSAR," Ph.D. Thesis, Umea, Sweden: University of Umea: 1986
	C24	"Vector NTI Suite 7.0 User's Manual (portion) describing software believed to be available prior to February 1, 2000
Examiner		Date Considered

Examiner: Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.